

## SEQUENCE LISTING

<110> Curtis, Rory A.J.

<120> 56201, A NOVEL HUMAN SODIUM ION CHANNEL  
FAMILY MEMBER AND USES THEREOF

<130> 10448-060001

<150> US 60/209,238

<151> 2000-06-05

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1356

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)...(1263)

<400> 1

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ggaaaatccc taagcagaga ttttctgttg gatgctaaaa gcaaggaata aaagttgaaa      60
atttggaata atg tct caa cac cgt cac cag cgc cac tcg aga gtc att tct      111
      Met Ser Gln His Arg His Gln Arg His Ser Arg Val Ile Ser
              1              5              10

agt tca cca gtt gac act aca tcg gtg gga ttt tgc cca aca ttc aag      159
Ser Ser Pro Val Asp Thr Thr Ser Val Gly Phe Cys Pro Thr Phe Lys
      15              20              25              30

aaa ttt aag agg aac gat gat gaa tgt cgg gca ttt gtg aag aga gtc      207
Lys Phe Lys Arg Asn Asp Asp Glu Cys Arg Ala Phe Val Lys Arg Val
              35              40              45

ata atg agc cgt ttc ttt aag ata att atg att agc act gtc aca tcg      255
Ile Met Ser Arg Phe Phe Lys Ile Ile Met Ile Ser Thr Val Thr Ser
              50              55              60

aat gcg ttt ttt atg gcc ttg tgg acc agt tat gac ata agg tac cgc      303
Asn Ala Phe Phe Met Ala Leu Trp Thr Ser Tyr Asp Ile Arg Tyr Arg
              65              70              75

ttg ttc aga ctt ctt gag ttc tcg gag atc ttc ttt gtg tcc atc tgc      351
Leu Phe Arg Leu Leu Glu Phe Ser Glu Ile Phe Phe Val Ser Ile Cys
              80              85              90

aca tct gag ttg tcc atg aag gtc tat gtg gac ccc atc aac tac tgg      399
Thr Ser Glu Leu Ser Met Lys Val Tyr Val Asp Pro Ile Asn Tyr Trp
      95              100              105              110

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aag aac ggc tac aac ctg ctg gat gtg atc att atc atc gtt atg ttt	447
Lys Asn Gly Tyr Asn Leu Leu Asp Val Ile Ile Ile Ile Val Met Phe	
115 120 125	
tta ccc tat gcc ctc cgc cag ctc atg ggc aaa cag ttc act tac ctg	495
Leu Pro Tyr Ala Leu Arg Gln Leu Met Gly Lys Gln Phe Thr Tyr Leu	
130 135 140	
tat atc gct gat ggc atg cag tcc ctg cgc atc ctc aag ctt atc ggc	543
Tyr Ile Ala Asp Gly Met Gln Ser Leu Arg Ile Leu Lys Leu Ile Gly	
145 150 155	
tat agc cag ggc atc cgg acg ctg atc acc gcc gtg ggg cag aca gtc	591
Tyr Ser Gln Gly Ile Arg Thr Leu Ile Thr Ala Val Gly Gln Thr Val	
160 165 170	
tac acc gtg gcc tct gtg ctc ctc ctg ctc ttc ctc ctc atg tac atc	639
Tyr Thr Val Ala Ser Val Leu Leu Leu Leu Phe Leu Leu Met Tyr Ile	
175 180 185 190	
ttc gct atc ttg ggc ttc tgc ctg ttt gga tct cca gac aat ggt gac	687
Phe Ala Ile Leu Gly Phe Cys Leu Phe Gly Ser Pro Asp Asn Gly Asp	
195 200 205	
cat gat aac tgg ggg aac ctg gct gca gct ttt ttc acc ctc ttc agc	735
His Asp Asn Trp Gly Asn Leu Ala Ala Ala Phe Phe Thr Leu Phe Ser	
210 215 220	
ttg gcc acg gtt gat ggc tgg aca gac ctg cag aag cag ttg gac aat	783
Leu Ala Thr Val Asp Gly Trp Thr Asp Leu Gln Lys Gln Leu Asp Asn	
225 230 235	
cgg gaa ttt gct ttg agc cgg gca ttc acc atc atc ttc atc ttg ctc	831
Arg Glu Phe Ala Leu Ser Arg Ala Phe Thr Ile Ile Phe Ile Leu Leu	
240 245 250	
gcc tct ttc atc ttc ctc aac atg ttc gtg ggt gtg atg atc atg cac	879
Ala Ser Phe Ile Phe Leu Asn Met Phe Val Gly Val Met Ile Met His	
255 260 265 270	
aca gag gac tcc atc aga aag ttt gag cga gag ctg atg ttg gag cag	927
Thr Glu Asp Ser Ile Arg Lys Phe Glu Arg Glu Leu Met Leu Glu Gln	
275 280 285	
cag gag atg ctc atg gga gag aag cag gtg att ctg cag cgg cag cag	975
Gln Glu Met Leu Met Gly Glu Lys Gln Val Ile Leu Gln Arg Gln Gln	
290 295 300	
gag gag atc agc agg ctg atg cac ata cag aaa aat gct gac tgc aca	1023
Glu Glu Ile Ser Arg Leu Met His Ile Gln Lys Asn Ala Asp Cys Thr	
305 310 315	
agt ttc agt gag ctg gtg gag aac ttt aag aag acc ttg agc cac act	1071
Ser Phe Ser Glu Leu Val Glu Asn Phe Lys Lys Thr Leu Ser His Thr	
320 325 330	
gac cca atg gtc ttg gat gat ttt ggc act agc tta ccc ttc atc gat	1119

Asp Pro Met Val Leu Asp Asp Phe Gly Thr Ser Leu Pro Phe Ile Asp  
 335 340 345 350  
 atc tac ttt tcc act ctg gac tac cag gac aca act gtc cac aag ctt 1167  
 Ile Tyr Phe Ser Thr Leu Asp Tyr Gln Asp Thr Thr Val His Lys Leu  
 355 360 365  
 caa gag ctg tac tat gag atc gtg cat gtg ctg agc cta atg ctg gaa 1215  
 Gln Glu Leu Tyr Tyr Glu Ile Val His Val Leu Ser Leu Met Leu Glu  
 370 375 380  
 gac ttg ccc cag gag aag ccc cag tcc ttg gaa aag gtg gat gag aag 1263  
 Asp Leu Pro Gln Glu Lys Pro Gln Ser Leu Glu Lys Val Asp Glu Lys  
 385 390 395  
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&lt;210&gt; 2

&lt;211&gt; 398

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met Ser Gln His Arg His Gln Arg His Ser Arg Val Ile Ser Ser Ser  
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 Pro Val Asp Thr Thr Ser Val Gly Phe Cys Pro Thr Phe Lys Lys Phe  
 20 25 30  
 Lys Arg Asn Asp Asp Glu Cys Arg Ala Phe Val Lys Arg Val Ile Met  
 35 40 45  
 Ser Arg Phe Phe Lys Ile Ile Met Ile Ser Thr Val Thr Ser Asn Ala  
 50 55 60  
 Phe Phe Met Ala Leu Trp Thr Ser Tyr Asp Ile Arg Tyr Arg Leu Phe  
 65 70 75 80  
 Arg Leu Leu Glu Phe Ser Glu Ile Phe Phe Val Ser Ile Cys Thr Ser  
 85 90 95  
 Glu Leu Ser Met Lys Val Tyr Val Asp Pro Ile Asn Tyr Trp Lys Asn  
 100 105 110  
 Gly Tyr Asn Leu Leu Asp Val Ile Ile Ile Val Met Phe Leu Pro  
 115 120 125  
 Tyr Ala Leu Arg Gln Leu Met Gly Lys Gln Phe Thr Tyr Leu Tyr Ile  
 130 135 140  
 Ala Asp Gly Met Gln Ser Leu Arg Ile Leu Lys Leu Ile Gly Tyr Ser  
 145 150 155 160  
 Gln Gly Ile Arg Thr Leu Ile Thr Ala Val Gly Gln Thr Val Tyr Thr  
 165 170 175  
 Val Ala Ser Val Leu Leu Leu Leu Phe Leu Leu Met Tyr Ile Phe Ala  
 180 185 190  
 Ile Leu Gly Phe Cys Leu Phe Gly Ser Pro Asp Asn Gly Asp His Asp  
 195 200 205  
 Asn Trp Gly Asn Leu Ala Ala Ala Phe Phe Thr Leu Phe Ser Leu Ala  
 210 215 220  
 Thr Val Asp Gly Trp Thr Asp Leu Gln Lys Gln Leu Asp Asn Arg Glu  
 225 230 235 240  
 Phe Ala Leu Ser Arg Ala Phe Thr Ile Ile Phe Ile Leu Leu Ala Ser  
 245 250 255  
 Phe Ile Phe Leu Asn Met Phe Val Gly Val Met Ile Met His Thr Glu

	260		265		270										
Asp	Ser	Ile	Arg	Lys	Phe	Glu	Arg	Glu	Leu	Met	Leu	Glu	Gln	Gln	Glu
	275		280		285										
Met	Leu	Met	Gly	Glu	Lys	Gln	Val	Ile	Leu	Gln	Arg	Gln	Gln	Glu	Glu
	290		295		300										
Ile	Ser	Arg	Leu	Met	His	Ile	Gln	Lys	Asn	Ala	Asp	Cys	Thr	Ser	Phe
305			310		315										320
Ser	Glu	Leu	Val	Glu	Asn	Phe	Lys	Lys	Thr	Leu	Ser	His	Thr	Asp	Pro
	325		330		335										
Met	Val	Leu	Asp	Asp	Phe	Gly	Thr	Ser	Leu	Pro	Phe	Ile	Asp	Ile	Tyr
	340		345		350										
Phe	Ser	Thr	Leu	Asp	Tyr	Gln	Asp	Thr	Thr	Val	His	Lys	Leu	Gln	Glu
	355		360		365										
Leu	Tyr	Tyr	Glu	Ile	Val	His	Val	Leu	Ser	Leu	Met	Leu	Glu	Asp	Leu
370			375		380										
Pro	Gln	Glu	Lys	Pro	Gln	Ser	Leu	Glu	Lys	Val	Asp	Glu	Lys		
385			390		395										

&lt;210&gt; 3

&lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

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gcatttgtga	agagagtcac	aatgagccgt	ttctttaaga	taattatgat	tagcactgtc	180
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agacttcttg	agttctcgga	gatcttcttt	gtgtccatct	gcacatctga	gttgtccatg	300
aaggtctatg	tggaccccat	caactactgg	aagaacggct	acaacctgct	ggatgtgatc	360
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cagggcatcc	ggacgctgat	caccgccgtg	gggcagacag	tctacaccgt	ggcctctgtg	540
ctcctcctgc	tcttcctcct	catgtacatc	ttcgctatct	tgggcttctg	cctgtttgga	600
tctccagaca	atggtgacca	tgataactgg	gggaacctgg	ctgcagcttt	tttcaccctc	660
ttcagcttgg	ccacggttga	tggctggaca	gacctgcaga	agcagttgga	caatcgggaa	720
tttgctttga	gccgggcatt	caccatcatc	ttcatcttgc	tcgcctcttt	catcttcctc	780
aacatgttcg	tgggtgtgat	gatcatgcac	acagaggact	ccatcagaaa	gtttgagcga	840
gagctgatgt	tggagcagca	ggagatgctc	atgggagaga	agcaggtgat	tctgcagcgg	900
cagcaggagg	agatcagcag	gctgatgcac	atacagaaaa	atgctgactg	cacaagtttc	960
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gattttggca	ctagcttacc	cttcatcgat	atctactttt	ccactctgga	ctaccaggac	1080
acaactgtcc	acaagcttca	agagctgtac	tatgagatcg	tgcagtgtgct	gagcctaata	1140
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&lt;210&gt; 4

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence

&lt;400&gt; 4

Ile	Val	Ser	Ser	Pro	Tyr	Phe	Glu	Leu	Phe	Ile	Leu	Leu	Thr	Ile	Leu
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Leu	Asn	Asp	Asp	Lys	Val	Ser	Lys	Thr	Ile	Ala	Leu	Ala	Met	Glu	His

			20					25					30						
Pro	Asn	Gln	Glu	Thr	Leu	Asn	Asp	Ile	Leu	Asp	Tyr	Val	Glu	Tyr	Val				
		35					40					45							
Phe	Thr	Gly	Ile	Phe	Thr	Phe	Glu	Met	Leu	Leu	Lys	Met	Ile	Ala	Leu				
	50					55					60								
Gly	Phe	Lys	Leu	His	Lys	Gly	Ala	Tyr	Phe	Arg	Asn	Gly	Trp	Asn	Ile				
65					70					75					80				
Leu	Asp	Phe	Val	Val	Val	Leu	Leu	Ser	Ile	Ile	Glu	Leu	Gly	Leu	Ser				
			85					90					95						
Leu	Ile	Asn	Lys	Lys	Ala	Ala	Asn	Val	Gly	Gly	Ser	Pro	Gln	Gln	Ala				
		100					105						110						
Lys	Gly	Ser	Leu	Phe	Gly	Leu	Lys	Val	Leu	Arg	Leu	Phe	Arg	Val	Leu				
	115						120					125							
Arg	Pro	Leu	Lys	Leu	Val	Arg	Arg	Ala	Pro	Gly	Leu	Arg	Val	Leu	Val				
	130					135					140								
Gln	Thr	Leu	Leu	Asn	Ser	Met	Lys	Ala	Leu	Gly	Asn	Leu	Leu	Leu	Leu				
145				150						155					160				
Leu	Phe	Leu	Phe	Val	Phe	Ile	Phe	Ala	Ile	Ile	Gly	Met	Gln	Leu	Phe				
			165						170				175						
Ala	Gly	Lys	Phe	Glu	Phe	Asp	Cys	Ile	Asp	Glu	Ser	Thr	Glu	Leu	Phe				
		180					185						190						
Asp	Ile	Ile	Ala	Thr	Glu	Pro	Ser	Leu	Cys	Gly	Asn	Glu	Ser	Tyr	Ala				
	195						200					205							
Arg	Asp	Cys	Pro	Asp	Gly	Tyr	Thr	Cys	Arg	Arg	Gly	Trp	Glu	Gly	Pro				
	210					215					220								
Asn	Asn	Gly	Arg	Thr	Asn	Phe	Asp	Asn	Phe	Pro	Gln	Ala	Phe	Leu	Thr				
225					230					235					240				
Leu	Phe	Gln	Val	Met	Thr	Gly	Glu	Gly	Trp	Gly	Asp	Val	Leu	Tyr	Asp				
			245						250					255					
Thr	Ile	Asp	Ala	Ala	Gly	Glu	Asp	Cys	Asp	Pro	Glu	Ser	Glu	Ala	Gly				
		260					265						270						
Gly	Gly	Ile	Cys	Gly	Asn	Asn	Val	Leu	Met	Gly	Ile	Tyr	Phe	Ile	Ser				
	275					280						285							
Leu	Ile	Ile	Leu	Gly	Ser	Phe	Leu	Thr	Leu	Asn	Leu	Phe	Leu	Ala	Val				
	290					295					300								
Ile																			
305																			

&lt;210&gt; 5

&lt;211&gt; 1836

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

Met	Ala	Arg	Pro	Ser	Leu	Cys	Thr	Leu	Val	Pro	Leu	Gly	Pro	Glu	Cys				
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Leu	Arg	Pro	Phe	Thr	Arg	Glu	Ser	Leu	Ala	Ala	Ile	Glu	Gln	Arg	Ala				
		20						25					30						
Val	Glu	Glu	Glu	Ala	Arg	Leu	Gln	Arg	Asn	Lys	Gln	Met	Glu	Ile	Glu				
	35						40					45							
Glu	Pro	Glu	Arg	Lys	Pro	Arg	Ser	Asp	Leu	Glu	Ala	Gly	Lys	Asn	Leu				
	50					55					60								
Pro	Met	Ile	Tyr	Gly	Asp	Pro	Pro	Pro	Glu	Val	Ile	Gly	Ile	Pro	Leu				
65					70					75					80				
Glu	Asp	Leu	Asp	Pro	Tyr	Tyr	Ser	Asn	Lys	Lys	Thr	Phe	Ile	Val	Leu				
			85					90					95						
Asn	Lys	Gly	Lys	Ala	Ile	Phe	Arg	Phe	Ser	Ala	Thr	Pro	Ala	Leu	Tyr				

			100				105					110			
Leu	Leu	Ser	Pro	Phe	Ser	Val	Val	Arg	Arg	Gly	Ala	Ile	Lys	Val	Leu
		115					120					125			
Ile	His	Ala	Leu	Phe	Ser	Met	Phe	Ile	Met	Ile	Thr	Ile	Leu	Thr	Asn
	130					135					140				
Cys	Val	Phe	Met	Thr	Met	Ser	Asp	Pro	Pro	Pro	Trp	Ser	Lys	Asn	Val
145					150					155					160
Glu	Tyr	Thr	Phe	Thr	Gly	Ile	Tyr	Thr	Phe	Glu	Ser	Leu	Ile	Lys	Ile
			165						170					175	
Leu	Ala	Arg	Gly	Phe	Cys	Val	Asp	Asp	Phe	Thr	Phe	Leu	Arg	Asp	Pro
		180						185					190		
Trp	Asn	Trp	Leu	Asp	Phe	Ser	Val	Ile	Met	Met	Ala	Tyr	Leu	Thr	Glu
	195						200					205			
Phe	Val	Asp	Leu	Gly	Asn	Ile	Ser	Ala	Leu	Arg	Thr	Phe	Arg	Val	Leu
	210				215						220				
Arg	Ala	Leu	Lys	Thr	Ile	Thr	Val	Ile	Pro	Gly	Leu	Lys	Thr	Ile	Val
225					230					235					240
Gly	Ala	Leu	Ile	Gln	Ser	Val	Lys	Lys	Leu	Ser	Asp	Val	Met	Ile	Leu
			245					250						255	
Thr	Val	Phe	Cys	Leu	Ser	Val	Phe	Ala	Leu	Val	Gly	Leu	Gln	Leu	Phe
		260						265					270		
Met	Gly	Asn	Leu	Arg	Gln	Lys	Cys	Val	Arg	Trp	Pro	Pro	Pro	Phe	Asn
	275						280					285			
Asp	Thr	Asn	Thr	Thr	Trp	Tyr	Ser	Asn	Asp	Thr	Trp	Tyr	Gly	Asn	Asp
	290					295					300				
Thr	Trp	Tyr	Gly	Asn	Glu	Met	Trp	Tyr	Gly	Asn	Asp	Ser	Trp	Tyr	Ala
305					310					315					320
Asn	Asp	Thr	Trp	Asn	Ser	His	Ala	Ser	Trp	Ala	Thr	Asn	Asp	Thr	Phe
			325					330						335	
Asp	Trp	Asp	Ala	Tyr	Ile	Ser	Asp	Glu	Gly	Asn	Phe	Tyr	Phe	Leu	Glu
		340					345					350			
Gly	Ser	Asn	Asp	Ala	Leu	Leu	Cys	Gly	Asn	Ser	Ser	Asp	Ala	Gly	His
	355						360					365			
Cys	Pro	Gln	Gly	Tyr	Glu	Cys	Ile	Lys	Thr	Gly	Arg	Asn	Pro	Asn	Tyr
	370					375					380				
Gly	Tyr	Thr	Ser	Tyr	Asp	Thr	Phe	Ser	Trp	Ala	Phe	Leu	Ala	Leu	Phe
385					390					395					400
Arg	Leu	Met	Thr	Gln	Asp	Tyr	Trp	Glu	Asn	Leu	Phe	Gln	Leu	Thr	Leu
			405					410						415	
Arg	Ala	Ala	Gly	Lys	Thr	Tyr	Met	Ile	Phe	Phe	Val	Val	Ile	Ile	Phe
		420						425					430		
Leu	Gly	Ser	Phe	Tyr	Leu	Ile	Asn	Leu	Ile	Leu	Ala	Val	Val	Ala	Met
	435						440					445			
Ala	Tyr	Ala	Glu	Gln	Asn	Glu	Ala	Thr	Leu	Ala	Glu	Asp	Lys	Glu	Lys
	450					455					460				
Glu	Glu	Glu	Phe	Gln	Gln	Met	Leu	Glu	Lys	Phe	Lys	Lys	His	Gln	Glu
465					470					475					480
Glu	Leu	Glu	Lys	Ala	Lys	Ala	Ala	Gln	Ala	Leu	Glu	Gly	Gly	Glu	Ala
			485					490						495	
Asp	Gly	Asp	Pro	Ala	His	Gly	Lys	Asp	Cys	Asn	Gly	Ser	Leu	Asp	Thr
		500						505					510		
Ser	Gln	Gly	Glu	Lys	Gly	Ala	Pro	Arg	Gln	Ser	Gly	Ser	Gly	Asp	Ser
	515						520					525			
Gly	Ile	Ser	Asp	Ala	Met	Glu	Glu	Leu	Glu	Glu	Ala	His	Gln	Lys	Cys
	530					535					540				
Pro	Pro	Trp	Trp	Tyr	Lys	Cys	Ala	His	Lys	Val	Leu	Ile	Trp	Asn	Cys
545					550					555					560

Cys	Ala	Pro	Trp	Leu	Lys	Phe	Lys	Asn	Ile	Ile	His	Leu	Ile	Val	Met	565	570	575
Asp	Pro	Phe	Val	Asp	Leu	Gly	Ile	Thr	Ile	Cys	Ile	Val	Leu	Asn	Thr	580	585	590
Leu	Phe	Met	Ala	Met	Glu	His	Tyr	Pro	Met	Thr	Glu	His	Phe	Asp	Asn	595	600	605
Val	Leu	Thr	Val	Gly	Asn	Leu	Val	Phe	Thr	Gly	Ile	Phe	Thr	Ala	Glu	610	615	620
Met	Val	Leu	Lys	Leu	Ile	Ala	Met	Asp	Pro	Tyr	Glu	Tyr	Phe	Gln	Gln	625	630	635
Gly	Trp	Asn	Ile	Phe	Asp	Ser	Ile	Ile	Val	Thr	Leu	Ser	Leu	Val	Glu	645	650	655
Leu	Gly	Leu	Ala	Asn	Val	Gln	Gly	Leu	Ser	Val	Leu	Arg	Ser	Phe	Arg	660	665	670
Leu	Leu	Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	Asn	Met	675	680	685
Leu	Ile	Lys	Ile	Ile	Gly	Asn	Ser	Val	Gly	Ala	Leu	Gly	Asn	Leu	Thr	690	695	700
Leu	Val	Leu	Ala	Ile	Ile	Val	Phe	Ile	Phe	Ala	Val	Val	Gly	Met	Gln	705	710	715
Leu	Phe	Gly	Lys	Ser	Tyr	Lys	Glu	Cys	Val	Cys	Lys	Ile	Ala	Leu	Asp	725	730	735
Cys	Asn	Leu	Pro	Arg	Trp	His	Met	His	Asp	Phe	Phe	His	Ser	Phe	Leu	740	745	750
Ile	Val	Phe	Arg	Ile	Leu	Cys	Gly	Glu	Trp	Ile	Glu	Thr	Met	Trp	Asp	755	760	765
Cys	Met	Glu	Val	Ala	Gly	Gln	Ala	Met	Cys	Leu	Thr	Val	Phe	Leu	Met	770	775	780
Val	Met	Val	Ile	Gly	Asn	Leu	Val	Val	Leu	Asn	Leu	Phe	Leu	Ala	Leu	785	790	795
Leu	Leu	Ser	Ser	Phe	Ser	Ala	Asp	Ser	Leu	Ala	Ala	Ser	Asp	Glu	Asp	805	810	815
Gly	Glu	Met	Asn	Asn	Leu	Gln	Ile	Ala	Ile	Gly	Arg	Ile	Lys	Leu	Gly	820	825	830
Ile	Gly	Phe	Ala	Lys	Ala	Phe	Leu	Leu	Gly	Leu	Leu	His	Gly	Lys	Ile	835	840	845
Leu	Ser	Pro	Lys	Asp	Ile	Met	Leu	Ser	Leu	Gly	Glu	Ala	Asp	Gly	Ala	850	855	860
Gly	Glu	Ala	Gly	Glu	Gly	Gly	Glu	Thr	Ala	Pro	Glu	Asp	Glu	Lys	Lys	865	870	875
Glu	Pro	Pro	Glu	Glu	Asp	Leu	Lys	Lys	Asp	Asn	His	Ile	Leu	Asn	His	885	890	895
Met	Gly	Leu	Ala	Asp	Gly	Pro	Pro	Ser	Ser	Leu	Glu	Leu	Asp	His	Leu	900	905	910
Asn	Phe	Ile	Asn	Asn	Pro	Tyr	Leu	Thr	Ile	Gln	Val	Pro	Ile	Ala	Ser	915	920	925
Glu	Glu	Ser	Asp	Leu	Glu	Met	Pro	Thr	Glu	Glu	Glu	Thr	Asp	Thr	Phe	930	935	940
Ser	Glu	Pro	Glu	Asp	Ser	Lys	Lys	Pro	Pro	Gln	Pro	Leu	Tyr	Asp	Gly	945	950	955
Asn	Ser	Ser	Val	Cys	Ser	Thr	Ala	Asp	Tyr	Lys	Pro	Pro	Glu	Glu	Asp	965	970	975
Pro	Glu	Glu	Gln	Ala	Glu	Glu	Asn	Pro	Glu	Gly	Glu	Gln	Pro	Glu	Glu	980	985	990
Cys	Phe	Thr	Glu	Ala	Cys	Val	Gln	Arg	Trp	Pro	Cys	Leu	Tyr	Val	Asp	995	1000	1005
Ile	Ser	Gln	Gly	Arg	Gly	Lys	Lys	Trp	Trp	Thr	Leu	Arg	Arg	Ala	Cys			



1010	1015	1020
Phe Lys Ile Val Glu His Asn Trp Phe Glu Thr Phe Ile Val Phe Met		
1025	1030	1035
Ile Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Ile Glu		1040
	1045	1050
Gln Arg Arg Val Ile Arg Thr Ile Leu Glu Tyr Ala Asp Lys Val Phe		1055
	1060	1065
Thr Tyr Ile Phe Ile Met Glu Met Leu Leu Lys Trp Val Ala Tyr Gly		1070
	1075	1080
Phe Lys Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile		1085
	1090	1095
Val Asp Val Ser Ile Ile Ser Leu Val Ala Asn Trp Leu Gly Tyr Ser		1100
1105	1110	1115
Glu Leu Gly Pro Ile Lys Ser Leu Arg Thr Leu Arg Ala Leu Arg Pro		1120
	1125	1130
Leu Arg Ala Leu Ser Arg Phe Glu Gly Met Arg Val Val Val Lys Pro		1135
	1140	1145
Leu Leu Gly Ala Ile Pro Ser Ile Met Asn Val Leu Leu Val Cys Leu		1150
	1155	1160
Ile Phe Trp Leu Ile Phe Ser Ile Met Gly Val Asn Leu Phe Ala Gly		1165
	1170	1175
Lys Phe Tyr Tyr Cys Ile Asn Thr Thr Thr Ser Glu Arg Phe Asp Ile		1180
1185	1190	1195
Ser Glu Val Asn Asn Lys Ser Glu Cys Glu Ser Leu Met His Thr Gly		1200
	1205	1210
Gln Val Arg Trp Leu Asn Val Lys Val Asn Tyr Asp Asn Val Gly Leu		1215
	1220	1225
Gly Tyr Leu Ser Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp		1230
	1235	1240
Ile Met Tyr Ala Ala Val Asp Ser Arg Glu Lys Glu Glu Gln Pro Gln		1245
	1250	1255
Tyr Glu Val Asn Leu Tyr Met Tyr Leu Tyr Phe Val Ile Phe Ile Ile		1260
1265	1270	1275
Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile Asp		1280
	1285	1290
Asn Phe Asn Gln Gln Lys Lys Lys Leu Gly Gly Lys Asp Ile Phe Met		1295
	1300	1305
Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser		1310
	1315	1320
Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Gln Asn Lys Ile Gln Gly		1325
	1330	1335
Met Val Tyr Asp Leu Val Thr Lys Gln Ala Phe Asp Ile Thr Ile Met		1340
1345	1350	1355
Ile Leu Ile Cys Leu Asn Met Val Thr Met Met Val Glu Thr Asp Asp		1360
	1365	1370
Gln Ser Gln Leu Lys Val Asp Ile Leu Tyr Asn Ile Asn Met Ile Phe		1375
	1380	1385
Ile Ile Ile Phe Thr Gly Glu Cys Val Leu Lys Met Leu Ala Leu Arg		1390
	1395	1400
Gln Tyr Tyr Phe Thr Val Gly Trp Asn Ile Phe Asp Phe Val Val Val		1405
	1410	1415
Ile Leu Ser Ile Val Gly Leu Ala Leu Ser Asp Leu Ile Gln Lys Tyr		1420
1425	1430	1435
Phe Val Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly		1440
	1445	1450
Arg Val Leu Arg Leu Ile Arg Gly Ala Lys Gly Ile Arg Thr Leu Leu		1455
	1460	1465
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Phe Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu
      1475                      1480                      1485
Leu Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ser Asn Phe
      1490                      1495                      1500
Ala Tyr Val Lys Lys Glu Ser Gly Ile Asp Asp Met Phe Asn Phe Glu
1505                      1510                      1515                      1520
Thr Phe Gly Asn Ser Ile Ile Cys Leu Phe Glu Ile Thr Thr Ser Ala
      1525                      1530                      1535
Gly Trp Asp Gly Leu Leu Asn Pro Ile Leu Asn Ser Gly Pro Pro Asp
      1540                      1545                      1550
Cys Asp Pro Asn Leu Glu Asn Pro Gly Thr Ser Val Lys Gly Asp Cys
      1555                      1560                      1565
Gly Asn Pro Ser Ile Gly Ile Cys Phe Phe Cys Ser Tyr Ile Ile Ile
1570                      1575                      1580
Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Ile Ile Leu Glu Asn
1585                      1590                      1595                      1600
Phe Asn Val Ala Thr Glu Glu Ser Ser Glu Pro Leu Gly Glu Asp Asp
      1605                      1610                      1615
Phe Glu Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Asp Ala Thr
      1620                      1625                      1630
Gln Phe Ile Ala Tyr Ser Arg Leu Ser Asp Phe Val Asp Thr Leu Gln
      1635                      1640                      1645
Glu Pro Leu Arg Ile Ala Lys Pro Asn Lys Ile Lys Leu Ile Thr Leu
      1650                      1655                      1660
Asp Leu Pro Met Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu
1665                      1670                      1675                      1680
Phe Ala Leu Thr Lys Glu Val Leu Gly Asp Ser Gly Glu Met Asp Ala
      1685                      1690                      1695
Leu Lys Gln Thr Met Glu Glu Lys Phe Met Ala Ala Asn Pro Ser Lys
      1700                      1705                      1710
Val Ser Tyr Glu Pro Ile Thr Thr Thr Leu Lys Arg Lys His Glu Glu
      1715                      1720                      1725
Val Cys Ala Ile Lys Ile Gln Arg Ala Tyr Arg Arg His Leu Leu Gln
1730                      1735                      1740
Arg Ser Met Lys Gln Ala Ser Tyr Met Tyr Arg His Ser His Asp Gly
1745                      1750                      1755                      1760
Ser Gly Asp Asp Ala Pro Glu Lys Glu Gly Leu Leu Ala Asn Thr Met
      1765                      1770                      1775
Ser Lys Met Tyr Gly His Glu Asn Gly Asn Ser Ser Ser Pro Ser Pro
      1780                      1785                      1790
Glu Glu Lys Gly Glu Ala Gly Asp Ala Gly Pro Thr Met Gly Leu Met
      1795                      1800                      1805
Pro Ile Ser Pro Ser Asp Thr Ala Trp Pro Pro Ala Pro Pro Pro Gly
      1810                      1815                      1820
Gln Thr Val Arg Pro Gly Val Lys Glu Ser Leu Val
1825                      1830                      1835

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<213> Artificial Sequence

<220>
<223> exemplary motif

<221> VARIANT
<222> 2

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<223> Xaa = any amino acid

<221> VARIANT

<222> 3

<223> Xaa = Asp or Glu

<400> 6

Thr Xaa Xaa Gly Trp  
1 5

1

5